

appear. In HIV-1 there are currently approximately 100 mutations that are thought to be involved in the development of HIV-a therapeutic agent resistance. One such example is N88S, which causes *in vitro* hypersensitivity to amprenavir. See, e.g. Ziemann et al., *J. Virol.* 74(9):4414-9 (2000). A summary of mutations in the HIV genome correlated with drug resistance has been reported. Schinazi, R.F., Larder, B.A. & Meliors, J.W. 1997. *Int. Antiviral News.* 5, 129-142 (1997), herein incorporated by reference. Additionally, an electronic listing with mutations has also become available on the internet at sites such as hiv-web.lanl.gov or www.viralresistance.com. - -

IN THE CLAIMS

Please amend claims 1, 13, and 20 as follows:

1. (Amended) A method for predicting resistance of a pathogen to a therapeutic agent comprising:

- (a) providing a trained neural network that is trained using a training data set comprising members that correspond to at least one genetic mutation that correlates to a phenotypic change that causes a change in resistance of the pathogen to the therapeutic agent;
- (b) providing a determined genetic sequence from the pathogen; and
- (c) predicting resistance of the pathogen to the therapeutic agent using the determined genetic sequence and the trained neural network to identify at least one mutation of the determined genetic sequence that confers resistance to the therapeutic agent.